REMARKS

Claims 115-153, 158-166 and 168-231 are pending in this application. By this Supplemental Amendment, claims 220-231 are amended and new claims 232-344 are added. Support for the amendments and newly added claims is found throughout the Specification and no new matter is added.

Specifically, PCR assays for detection of polynucleotides is disclosed in section II.H pages 62-63 of the Specification. Use of polynucleotides representing HCV cDNA sequences for the detection of HCV is described in section II.J of the Specification (72:29-34). Oligonucleotide probes comprising 10 and 15 HCV nucleotides are disclosed in Section II.H, on page 61 (*see also*, Figures 58 and 89). Applications of the claimed methods in preparation of human blood-related products and polyclonal antibodies, and in passive immunotherapy are disclosed on page 8, page 41, in sections II.B, G, and I and throughout the Specification. Antigenic polypeptides of 10 contiguous amino acids are disclosed on page 27. ELISA and radioimmunoassays are disclosed in section II.I (pp. 64-68) of the Specification. Support for the newly added claims can be found in Figure 62 and 90 and their corresponding descriptions. Lambda gt-11 library of cDNA inserts deposited as ATCC No. 40394 is disclosed on page 255 of the Specification. Potential epitopes specified in claim 326 is disclosed on pages 51-52, and epitopes of claim 335 on page 152 of the Specification.

No new matter is added. Entry of amendments to claims 220-231 and new claims 232-344 is respectfully requested.

CONCLUSION

Applicants earnestly believe that they are entitled to a letters patent on the pending claims, and respectfully solicit the Examiner to expedite prosecution of this patent application to issuance. Should the Examiner have any questions, the Examiner is encouraged to telephone the

undersigned. If the Examiner determines that the claims are not allowable, Applicants request an opportunity to interview the Examiner.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned "**Version with markings to show changes made**".

In the unlikely event that the transmittal letter is separated from this document and the Patent Office determines that an extension and/or other relief is required, applicant petitions for any required relief including extensions of time and authorizes the Assistant Commissioner to charge the cost of such petitions and/or other fees due in connection with the filing of this document to **Deposit Account No. 03-1952** referencing docket no. 223002006313. However, the Assistant Commissioner is not authorized to charge the cost of the issue fee to the Deposit Account.

Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Claims:

220. (Amended) A method of selecting [biological]samples from a supply of biological samples comprising selecting from said supply those samples [that contain a detectable polynucleotide comprising]which comprise a first polynucleotide that is capable of hybridizing under stringent conditions to a second polynucleotide that comprises a contiguous sequence of at least 15 nucleotides from [either strand of at least one of the hepatitis C virus (HCV) cDNA inserts in a lambda gt-11 cDNA library deposited as ATCC No. 40394]the genome of a hepatitis C virus genome or the complement thereof.

221. (Amended) [The method according to claim 115, wherein the detectable polynucleotide comprises a contiguous sequence of less than about 90 nucleotides fully complementary to either strand of Figure 3] A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which do not comprise a first polynucleotide that is capable of hybridizing under stringent conditions to a second polynucleotide that comprises a contiguous sequence of at least 15 nucleotides from the genome of a hepatitis C virus genome or the complement thereof.

222. (Amended) [The method according to claim 116, wherein the detectable polynucleotide comprises a contiguous sequence of less than about 90 nucleotides fully complementary to either strand of Figure 62.] A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which comprise a first polynucleotide that is capable of hybridizing under stringent conditions to a second polynucleotide that comprises a contiguous sequence of at least 15 nucleotides from either strand of at least one of the HCV cDNA inserts in a lambda gt-11 cDNA library deposited as ATCC No. 40394.

223. (Amended) [The method according to claim 117, wherein the detectable polynucleotide comprises a contiguous sequence of less than about 90 nucleotides fully complementary to either strand of Figure 89]A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which do not comprise a first polynucleotide that is capable of hybridizing under stringent conditions to a second polynucleotide that comprises a contiguous sequence of at least 15 nucleotides from either strand of at least one of the HCV cDNA inserts in a lambda gt-11 cDNA library deposited as ATCC No. 40394.

224. (Amended) [The method according to claim 118, wherein the selected samples comprise a polynucleotide that hybridizes under stringent conditions to a polynucleotide that comprises a contiguous sequence of less than about 90 nucleotides from the genome of a hepatitis C virus genome or the complement thereof]A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which comprise a first polynucleotide that is capable of hybridizing under stringent conditions to a second polynucleotide that comprises a contiguous sequence of at least 15 nucleotides found in Figure 89, or the complement thereof.

225. (Amended) [The method according to claim 119, wherein the selected samples comprise a polynucleotide that hybridizes under stringent conditions to a contiguous sequence of less than about 90 nucleotides from either strand of at least one of the hepatitis C virus (HCV) cDNA inserts in a lambda gt-11 cDNA library deposited as ATCC No. 40394]A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which do not comprise a first polynucleotide that is capable of hybridizing

under stringent conditions to a second polynucleotide that comprises a contiguous sequence of at least 15 nucleotides found in Figure 89, or the complement thereof.

226. (Amended) [The method according to claim 120, wherein the selected samples comprise a polynucleotide that hybridizes under stringent conditions to a contiguous sequence of less than about 90 nucleotides fully complementary to either strand of Figure 89]A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which comprise a first polynucleotide that is capable of hybridizing under stringent conditions to a second polynucleotide that comprises a contiguous sequence of at least 15 nucleotides found in either strand of Figure 58.

227. (Amended) [The method according to claim 121, wherein the selected samples comprise a polynucleotide that hybridizes under stringent conditions to a contiguous sequence of less than about 90 nucleotides fully complementary to either strand of Figure 14]A method of selecting samples from a supply of human biological samples comprising selecting from said supply those samples which do not comprise a first polynucleotide that is capable of hybridizing under stringent conditions to a second polynucleotide that comprises a contiguous sequence of at least 15 nucleotides found in either stand of Figure 58.

228. (Amended) [The method according to claim 115, wherein the detectable polynucleotide comprises a contiguous sequence of less than about 90 nucleotides from either strand of at least one of the hepatitis C virus (HCV) cDNA inserts in a lambda gt-11 cDNA library deposited as ATCC No. 40394]A method according to any of claims 220, 222, 224, or 226 wherein said selected samples comprise said first polynucleotide and said stringent conditions permit the formation of a stable hybrid duplex between said first polynucleotide and

said contiguous sequence of nucleotides and do not permit the formation of a stable duplex between said contiguous sequence and the genomes of Hepatitis B or Hepatitis A viruses.

229. (Amended) [The method according to claim 126, wherein said stringent conditions include using a hybridization solution comprising 50% (w/v) formamide and washing in 5x SSC, 0.1% SDS at 55°C]A method according to any of claims 221, 223, 225 or 227 wherein said selected samples do not comprise said first polynucleotide and said stringent conditions permit the formation of a stable hybrid duplex between said first polynucleotide and said contiguous sequence and do not permit the formation of a stable duplex between said contiguous sequence and the genomes of Hepatitis B or Hepatitis A viruses.

230. (Amended) A method according to claim [126]228, wherein said stringent conditions include using 50% (w/v) formamide and washing in 5xSSC, 0.1% SDS at 55 °C.

231. (Amended) A method [of selecting samples from a supply of human biological samples comprising selecting from said supply those samples that comprise a first polynucleotide that is capable of hybridizing under stringent conditions to a second polynucleotide that comprises a contiguous sequence of at least 15 nucleotides found in Figure 89 or complement thereof]according to claim 229, wherein said stringent conditions include using 50% (w/v) formamide and washing in 5xSSC, 0.1% SDS at 55 °C.

Claims 232-344 are newly added.